



SEQUENCE LISTING

<10> DeBonte, Lorin R.
Fan, Zhegong
Miao, Guo-Hua

<120> PLANTS HAVING MUTANT SEQUENCES THAT
CONFER ALTERED FATTY ACID PROFILES

<130> 07148-032001

<140> US 08/572,027

<141> 1995-12-14

<160> 50

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1155

<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (1)...(1152)

<223> wild type D form

<221> misc_feature

<222> 205

<223> n = A,T,C or G

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gaa acc gac acc atc aag cgc gta ccc tgc gag aca ccg ccc ttc act	96
Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr	
20 25 30	

gtc gga gaa ctc aag aaa gca atc cca ccg cac tgt ttc aaa cgc tcg	144
Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser	
35 40 45	

atc cct cgc tct ttc tcc tac ctc atc tgg gac atc atc ata gcc tcc	192
Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser	
50 55 60	

tgc ttc tac tac ntc gcc acc act tac ttc cct ctc ctc cct cac cct	240
Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro	
65 70 75 80	

ctc tcc tac ttc gcc tgg cct ctc tac tgg gcc tgc caa ggg tgc gtc	288
Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val	
85 90 95	

cta acc ggc gtc tgg gtc ata gcc cac gaa tgc ggc cac cac gcc ttc	336
Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe	
100 105 110	
agc gac tac cag tgg ctt gac gac acc gtc ggt ctc atc ttc cac tcc	384
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser	
115 120 125	
ttc ctc ctc gtc cct tac ttc tcc tgg aag tac agt cat cgc agc cac	432
Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His	
130 135 140	
cat tcc aac act ggc tcc ctc gag aga gac gaa gtg ttt gtc ccc aag	480
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys	
145 150 155 160	
aag aag tca gac atc aag tgg tac ggc aag tac ctc aac aac cct ttg	528
Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu	
165 170 175	
gga cgc acc gtg atg tta acg gtt cag ttc act ctc ggc tgg ccg ttg	576
Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu	
180 185 190	
tac tta gcc ttc aac gtc tcg gga aga cct tac gac ggc ggc ttc cgt	624
Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg	
195 200 205	
tgc cat ttc cac ccc aac gct ccc atc tac aac gac cgc gag cgt ctc	672
Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu	
210 215 220	
cag ata tac atc tcc gac gct ggc atc ctc gcc gtc tgc tac ggt ctc	720
Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu	
225 230 235 240	
ttc cgt tac gcc gcc ggc cag gga gtg gcc tcg atg gtc tgc ttc tac	768
Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr	
245 250 255	
gga gtc ccg ctt ctg att gtc aat ggt ttc ctc gtg ttg atc act tac	816
Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr	
260 265 270	
ttg cag cac acg cat cct tcc ctg cct cac tac gat tcg tcc gag tgg	864
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp	
275 280 285	
gat tgg ttc agg gga gct ttg gct acc gtt gac aga gac tac gga atc	912
Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile	
290 295 300	
ttg aac aag gtc ttc cac aat att acc gac acg cac gtg gcc cat cat	960
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His	
305 310 315 320	

ccg ttc tcc acg atg ccg cat tat cac gcg atg gaa gct acc aag gcg 1008
 Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
 325 330 335

ata aag ccg ata ctg gga gag tat tat cag ttc gat ggg acg ccg gtg 1056
 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
 340 345 350

gtt aag gcg atg tgg agg gag gcg aag gag tgt atc tat gtg gaa ccg 1104
 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
 355 360 365

gac agg caa ggt gag aag aaa ggt gtg ttc tgg tac aac aat aag tta 1152
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tga 1155

<210> 2

<211> 384

<212> PRT

<213> Brassica napus

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<222> 69

<223> Xaa = Any Amino Acid

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 35 40 45
 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ala Ser
 50 55 60
 Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
 65 70 75 80
 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
 85 90 95
 Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
 100 105 110
 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
 115 120 125
 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His
 130 135 140
 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
 145 150 155 160
 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
 165 170 175
 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
 180 185 190
 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg
 195 200 205
 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
 210 215 220

Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
 225 230 235 240
 Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr
 245 250 255
 Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr
 260 265 270
 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp
 275 280 285
 Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
 290 295 300
 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
 305 310 315 320
 Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
 325 330 335
 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
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 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
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<210> 3

<211> 1155

<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (1)...(1152)

<223> Clone: IMC129, G to A transversion mutation at
nucleotide 316 of the D form

<221> misc_feature

<222> 205

<223> n = A,T,C or G

<400> 3

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 gaa acc gac acc atc aag cgc gta ccc tgc gag aca ccg ccc ttc act	96
Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr	
20 25 30	
 gtc gga gaa ctc aag aaa gca atc cca ccg cac tgt ttc aaa cgc tcg	144
Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser	
35 40 45	
 atc cct cgc tct ttc tcc tac ctc atc tgg gac atc atc ata gcc tcc	192
Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser	
50 55 60	
 tgc ttc tac tac ntc gcc acc act tac ttc cct ctc ctc cct cac cct	240
Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro	
65 70 75 80	

ctc tcc tac ttc gcc tgg cct ctc tac tgg gcc tgc caa ggg tgc gtc	288
Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val	
85 90 95	
cta acc ggc gtc tgg gtc ata gcc cac aag tgc ggc cac cac gcc ttc	336
Leu Thr Gly Val Trp Val Ile Ala His Lys Cys Gly His His Ala Phe	
100 105 110	
agc gac tac cag tgg ctt gac gac acc gtc ggt ctc atc ttc cac tcc	384
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser	
115 120 125	
ttc ctc ctc gtc cct tac ttc tcc tgg aag tac agt cat cgc agc cac	432
Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His	
130 135 140	
cat tcc aac act ggc tcc ctc gag aga gac gaa gtg ttt gtc ccc aag	480
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys	
145 150 155 160	
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Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu	
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gga cgc acc gtg atg tta acg gtt cag ttc act ctc ggc tgg ccg ttg	576
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Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg	
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tgc cat ttc cac ccc aac gct ccc atc tac aac gac cgc gag cgt ctc	672
Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu	
210 215 220	
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Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu	
225 230 235 240	
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Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr	
245 250 255	
gga gtc ccg ctt ctg att gtc aat ggt ttc ctc gtg ttg atc act tac	816
Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr	
260 265 270	
ttg cag cac acg cat cct tcc ctg cct cac tac gat tcg tcc gag tgg	864
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp	
275 280 285	
gat tgg ttc agg gga gct ttg gct acc gtt gac aga gac tac gga atc	912
Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile	
290 295 300	
ttg aac aag gtc ttc cac aat att acc gac acg cac gtg gcc cat cat	960

Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
 305 310 315 320

ccg ttc tcc acg atg ccg cat tat cac gcg atg gaa gct acc aag gcg 1008
 Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
 325 330 335

ata aag ccg ata ctg gga gag tat tat cag ttc gat ggg acg ccg gtg 1056
 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
 340 345 350

gtt aag gcg atg tgg agg gag gcg aag gag tgt atc tat gtg gaa ccg 1104
 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
 355 360 365

gac agg caa ggt gag aag aaa ggt gtg ttc tgg tac aac aat aag tta 1152
 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
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tga 1155

<210> 4
 <211> 384
 <212> PRT
 <213> Brassica napus

<220>
 <221> VARIANT
 <222> 69
 <223> Xaa = Any Amino Acid

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 Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
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 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
 35 40 45
 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ala Ser
 50 55 60
 Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
 65 70 75 80
 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
 85 90 95
 Leu Thr Gly Val Trp Val Ile Ala His Lys Cys Gly His His Ala Phe
 100 105 110
 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
 115 120 125
 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His
 130 135 140
 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
 145 150 155 160
 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
 165 170 175
 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
 180 185 190

Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg
 195 200 205
 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
 210 215 220
 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
 225 230 235 240
 Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr
 245 250 255
 Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr
 260 265 270
 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp
 275 280 285
 Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
 290 295 300
 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
 305 310 315 320
 Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
 325 330 335
 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
 340 345 350
 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
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 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
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<210> 5

<211> 1155

<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (1)...(1152)

<223> wild type F form

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 Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
 20 25 30

gtc gga gaa ctc aag aaa gca atc cca ccg cac tgt ttc aaa cgc tcg 144
 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
 35 40 45

atc cct cgc tct ttc tcc tac ctc atc tgg gac atc atc ata gcc tcc 192
 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser
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tgc ttc tac tac gtc gcc acc act tac ttc cct ctc ctc cct cac cct 240
 Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
 65 70 75 80

ctc tcc tac ttc gcc tgg cct ctc tac tgg gcc tgc cag ggc tgc gtc	288
Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val	
85 90 95	
cta acc ggc gtc tgg gtc ata gcc cac gag tgc ggc cac cac gcc ttc	336
Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe	
100 105 110	
agc gac tac cag tgg ctg gac gac acc gtc ggc ctc atc ttc cac tcc	384
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser	
115 120 125	
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Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His	
130 135 140	
cat tcc aac act ggc tcc ctc gag aga gac gaa gtg ttt gtc ccc aag	480
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys	
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aag aag tca gac atc aag tgg tac ggc aag tac ctc aac aac cct ttg	528
Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu	
165 170 175	
gga cgc acc gtg atg tta acg gtt cag ttc act ctc ggc tgg cct ttg	576
Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu	
180 185 190	
tac tta gcc ttc aac gtc tcg ggg aga cct tac gac ggc ggc ttc gct	624
Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala	
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tgc cat ttc cac ccc aac gct ccc atc tac aac gac cgc gag cgt ctc	672
Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu	
210 215 220	
cag ata tac atc tcc gac gct ggc atc ctc gcc gtc tgc tac ggt ctc	720
Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu	
225 230 235 240	
tac cgc tac gct gct gtc caa gga gtt gcc tcg atg gtc tgc ttc tac	768
Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr	
245 250 255	
gga gtt ccg ctt ctg att gtc aat ggg ttc tta gtt ttg atc act tac	816
Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr	
260 265 270	
ttg cag cac acg cat cct tcc ctg cct cac tat gac tcg tct gag tgg	864
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp	
275 280 285	
gat tgg ttg agg gga gct ttg gcc acc gtt gac aga gac tac gga atc	912
Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile	
290 295 300	

ttg aac aag gtc ttc cac aat atc acg gac acg cac gtg gcg cat cac 960
 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
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ctg ttc tcg acc atg ccg cat tat cat gcg atg gaa gct acg aag gcg 1008
 Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
 325 330 335

ata aag ccg ata ctg gga gag tat tat cag ttg cat ggg acg ccg gtg 1056
 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Leu His Gly Thr Pro Val
 340 345 350

gtt aag gcg atg tgg agg gag gcg aag gag tgt atc tat gtg gaa ccg 1104
 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
 355 360 365

gac agg caa ggt gag aag aaa ggt gtg ttc tgg tac aac aat aag tta 1152
 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
 370 375 380

tga 1155

<210> 6

<211> 384

<212> PRT

<213> Brassica napus

<400> 6

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 35 40 45
 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ala Ser
 50 55 60
 Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
 65 70 75 80
 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
 85 90 95
 Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
 100 105 110
 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
 115 120 125
 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
 130 135 140
 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
 145 150 155 160
 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
 165 170 175
 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
 180 185 190
 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala
 195 200 205
 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
 210 215 220

Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
 225 230 235 240
 Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr
 245 250 255
 Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr
 260 265 270
 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp
 275 280 285
 Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
 290 295 300
 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
 305 310 315 320
 Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
 325 330 335
 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Leu His Gly Thr Pro Val
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<210> 7

<211> 1155

<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (1)...(1152)

<223> Clone: Q508, T to A transversion mutation at
nucleotide 515 of the F form

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 Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
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gtc gga gaa ctc aag aaa gca atc cca ccg cac tgt ttc aaa cgc tcg 144
 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
 35 40 45

atc cct cgc tct ttc tcc tac ctc atc tgg gac atc atc ata gcc tcc 192
 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser
 50 55 60

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 Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
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ctc tcc tac ttc gcc tgg cct ctc tac tgg gcc tgc cag ggc tgc gtc 288
 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
 85 90 95

cta acc ggc gtc tgg gtc ata gcc cac gag tgc ggc cac cac gcc ttc	336
Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe	
100 105 110	
agc gac tac cag tgg ctg gac gac acc gtc ggc ctc atc ttc cac tcc	384
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser	
115 120 125	
ttc ctc ctc gtc cct tac ttc tcc tgg aag tac agt cat cga cgc cac	432
Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His	
130 135 140	
cat tcc aac act ggc tcc ctc gag aga gac gaa gtg ttt gtc ccc aag	480
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys	
145 150 155 160	
aag aag tca gac atc aag tgg tac ggc aag tac cac aac aac cct ttg	528
Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr His Asn Asn Pro Leu	
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gga cgc acc gtg atg tta acg gtt cag ttc act ctc ggc tgg cct ttg	576
Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu	
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Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala	
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Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu	
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Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu	
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Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr	
245 250 255	
gga gtt ccg ctt ctg att gtc aat ggg ttc tta gtt ttg atc act tac	816
Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr	
260 265 270	
ttg cag cac acg cat cct tcc ctg cct cac tat gac tcg tct gag tgg	864
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp	
275 280 285	
gat tgg ttg agg gga gct ttg gcc acc gtt gac aga gac tac gga atc	912
Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile	
290 295 300	
ttg aac aag gtc ttc cac aat atc acg gac acg cac gtg gcg cat cac	960
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His	
305 310 315 320	

ctg ttc tcg acc atg ccg cat tat cat gcg atg gaa gct acg aag gcg 1008
 Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
 325 330 335

ata aag ccg ata ctg gga gag tat tat cag ttg cat ggg acg ccg gtg 1056
 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Leu His Gly Thr Pro Val
 340 345 350

gtt aag gcg atg tgg agg gag gcg aag gag tgt atc tat gtg gaa ccg 1104
 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
 355 360 365

gac agg caa ggt gag aag aaa ggt gtg ttc tgg tac aac aat aag tta 1152
 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
 370 375 380

tga 1155

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 Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
 20 25 30
 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
 35 40 45
 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser
 50 55 60
 Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
 65 70 75 80
 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
 85 90 95
 Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
 100 105 110
 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
 115 120 125
 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
 130 135 140
 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
 145 150 155 160
 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr His Asn Asn Pro Leu
 165 170 175
 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
 180 185 190
 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala
 195 200 205
 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
 210 215 220
 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
 225 230 235 240
 Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr
 245 250 255

Gly	Val	Pro	Leu	Leu	Ile	Val	Asn	Gly	Phe	Leu	Val	Leu	Ile	Thr	Tyr
			260					265					270		
Leu	Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Ser	Glu	Trp
		275					280					285			
Asp	Trp	Leu	Arg	Gly	Ala	Leu	Ala	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile
	290					295				300					
Leu	Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His
305					310					315					320
Leu	Phe	Ser	Thr	Met	Pro	His	Tyr	His	Ala	Met	Glu	Ala	Thr	Lys	Ala
			325						330					335	
Ile	Lys	Pro	Ile	Leu	Gly	Glu	Tyr	Tyr	Gln	Leu	His	Gly	Thr	Pro	Val
		340					345					350			
Val	Lys	Ala	Met	Trp	Arg	Glu	Ala	Lys	Glu	Cys	Ile	Tyr	Val	Glu	Pro
		355					360					365			
Asp	Arg	Gln	Gly	Glu	Lys	Lys	Gly	Val	Phe	Trp	Tyr	Asn	Asn	Lys	Leu
	370					375					380				

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His Lys Cys Gly His
1 5

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His Arg Arg His His
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<210> 14

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<212> PRT

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Lys Tyr His Asn Asn

1 5

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<213> Arabidopsis thaliana

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Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser Phe

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<213> Glycine max

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<212> PRT

<213> Zea mays

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Ser Leu Leu Asp Asp Val Val Gly Leu Val Leu His Ser Ser

20 25 30

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<212> PRT

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<400> 18

Trp Val Met Ala His Asp Cys Gly His His Ala Phe Ser Asp Tyr Gln

1 5 10 15

Leu Leu Asp Asp Val Val Gly Leu Ile Leu His Ser Cys

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 <213> Brassica napus

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 Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val
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 20 25 30
 Met Glu Ala Thr
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<400> 27
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 1 5 10 15
 Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr His Ala
 20 25 30
 Met Glu Ala Thr
 35

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Thr Gln Val Ala His His Leu Phe Thr Met Pro
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 Thr His Val Ala His His Pro Phe Ser Thr Met Pro His Tyr His Ala
 20 25 30
 Met Glu Ala Thr
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1				5				10						15	
Asn	Asp	Pro	Lys	Leu	Asn										
				20											

<210> 36

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<213> Brassica napus

<400> 36

Trp	Ala	Leu	Phe	Val	Leu	Gly	His	Asp	Cys	Gly	His	Gly	Ser	Phe	Ser
1				5				10						15	
Asn	Asp	Pro	Arg	Leu	Asn										
				20											

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<400> 37

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1				5				10						15	
Asn	Asn	Ser	Lys	Leu	Asn										
				20											

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<400> 38

Trp	Ala	Ile	Phe	Val	Leu	Gly	His	Asp	Cys	Gly	His	Gly	Ser	Phe	Ser
1				5				10						15	
Asp	Ile	Pro	Leu	Leu	Asn										
				20											

<210> 39

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<400> 39

Trp Ala Leu Phe Val Leu Gly His Asp Cys Gly His Gly Ser Phe Ser
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 Asp Ser Pro Pro Leu Asn
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<212> PRT

<213> Brassica napus

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Ala His Lys Cys Gly His
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<400> 41

Ala His Glu Cys Gly His
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Gly His Asp Cys Ala His
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<400> 43

Gly His Asp Cys Gly His
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21

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21

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1

5

10

15

Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr His Ala

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25

30

Met Glu Ala Thr

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